

In the Specification:

Please amend the specification as shown:

Please delete the paragraph on page 27, line 30 to page 28, line 13 and replace it with the following paragraph:

Polypeptides in the EGF family appear, in some ways, unrelated. For example, TGF α and EGF have only 30% structural homology (Marquardt *et al.*, *Science* 223:1079-1082, 1984). However, they display similar binding kinetics for, and stimulate tyrosine-specific phosphorylation of, the M_r 180,000 EGF membrane receptor (Cohen *et al.*, *J. Biol. Chem.* 255:4834-4842, 1980; Reynolds *et al.*, *Nature* 292:259-262, 1981). The functional equivalence of the two growth factors is partly attributed to the same relative positioning of six cysteine residues, represented by "C" in the consensus sequence: CX₇CX_{4,5}CX₁₀CXCX₈C (**SEQ ID NO: 1**). These conserved residues impose similar disulfide bond-mediated structural constraints and, thus, a related three-dimensional structure (Twardzik *et al.*, *Proc. Natl. Acad. Sci. USA* 82:5300-5304, 1985). Those of ordinary skill in the art are well able to compare any given amino acid sequence with the EGF-family consensus sequence to determine whether a polypeptide is likely to be functionally equivalent to EGF (and, if so, useful in practicing the methods of the present invention). (see, *e.g.*, Blomquist *et al.*, *Proc. Natl. Acad. Sci. USA* 81:7363-7367, 1984, for a description of a computer search that revealed a similar pattern of cysteine and glycine residues in EGF, TGF α , and the sequence of a 19 kDa early protein of vaccinia virus).